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Bonde, Ida; Lennen, Rebecca; Cardoso, Joao; Koza, Anna; Herrgard, Markus

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Analysis of gene essentiality in *Escherichia coli* across strains and growth conditions.

Ida Bonde, Rebecca Lennen, João Cardoso, Anna Koza, Markus Herrgård.

DTU Biosustain, Technical University of Denmark, Hørsholm, Denmark.

Different types of knock-out studies have for years been applied in addressing the question of gene essentiality in various organisms. The development within the field of next generation sequencing has paved the way for more extensive studies due to the high throughput. One of these fairly recent methods is transposon insertion sequencing (Tn-Seq), in which a mutant library is constructed by randomly inserting transposons into the genome, the position of which is determined by sequencing. By knowing the number of inserts in each gene in the initial library it is possible to determine if genes are either essential or detrimental for growth in the test condition in question. In this study the Tn-Seq method was used to investigate the differences in gene essentiality between four laboratory strains of *E. coli* subjected to four different growth conditions to investigate the reason for the differences in osmotic and chemical stress tolerance that exists between the strains as well as to assess the commonalities. Based on the sequencing data we identified genes that were essential for growth under the different conditions, some of which are essential in all conditions across strains and others that are specifically essential under certain growth conditions and/or in certain strains. This knowledge is important in the effort to engineer more stress tolerant strains, which are highly relevant for industrial purposes. Here is presented the bioinformatics analysis of the data, which includes one to one comparisons for each strain in each condition to the control condition and a multivariate analysis including all strains across conditions.

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Maternal airway exposure to TiO₂-nanoparticles: gene expression and promoter usage in the liver and placenta.

Mette Boyd, Morana Vitezic, Jette Bornholdt, Anne Thøustrup Saber, Ulla Vogel, Karin Sørig Hougaard, Albin Sandelin.

The Bioinformatics Centre and Biotech Research and Innovation Centre (BRIC), University of Copenhagen, and National Research Centre for the Working Environment, Denmark.

Maternal airway exposure to nanosized particles may interfere negatively with fetal development and affect organ function after birth. The placenta is the interface between mother and fetus, and has been suggested to be an important player in the transfer of effects of maternal exposure to particles to the fetus. In other words, the placenta has been hypothesized to adapt to the maternal environment in order to influence fetal development in a way that prepares the offspring for the environment later in life. To investigate the underlying molecular processes, we have generated genome-wide maps of active transcription start sites (TSSs) and enhancers in placenta, maternal and fetal liver tissue from pregnant mice with and without exposing the mice to nanoparticles (TiO₂, a common component of paints and sunscreen lotions). We identified a large number of active promoters and enhancers, many of which change expression in response to the TiO₂ exposure. Surprisingly, we find that maternal lung exposure leads to a rapid and dramatic down-regulation of gene expression in the placenta, while inducing pronounced up-regulation of inflammatory genes in maternal and embryonic liver.